



OIIPE

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/024,036B

DATE: 10/16/2002 P.6  
TIME: 15:51:30

Input Set : A:\Sequence listing.txt

Output Set: N:\CRF4\10162002\J024036B.raw

4 <110> APPLICANT: Bandaru, Rajasekhar  
 6 <120> TITLE OF INVENTION: 68730 and 69112, Protein Kinase  
 7 Molecules and Uses Therefor  
 11 <130> FILE REFERENCE: MPI2000-521P1R(M)  
 13 <140> CURRENT APPLICATION NUMBER: US/10/024,036B  
 14 <141> CURRENT FILING DATE: 2001-12-17  
 16 <150> PRIOR APPLICATION NUMBER: 60/258222  
 17 <151> PRIOR FILING DATE: 2000-12-22  
 19 <160> NUMBER OF SEQ ID NOS: 10  
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 1772  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Homo sapiens  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: 5'UTR  
 30 <222> LOCATION: (1)...(168)  
 32 <221> NAME/KEY: CDS  
 33 <222> LOCATION: (169)...(1242)  
 W--> 35 <221> 3'UTR  
 36 <222> LOCATION: (1243)...(1772)  
 W--> 38 <221> unsure  
 39 <222> LOCATION: 1  
 40 <223> OTHER INFORMATION: n may be A, T, G, or C.  
 W--> 42 <221> unsure  
 43 <222> LOCATION: 3  
 44 <223> OTHER INFORMATION: n may be A, T, G, or C.  
 W--> 46 <221> unsure  
 47 <222> LOCATION: 5  
 48 <223> OTHER INFORMATION: n may be A, T, G, or C.  
 W--> 50 <221> unsure  
 51 <222> LOCATION: (6)...(6)  
 52 <223> OTHER INFORMATION: n may be A, T, G, or C.  
 W--> 54 <400> 1  
 W--> 55 ncngnncgcg gcggcgtgcg cactgagcgaa agaggaaact gcagaggagg aagctgcgcc 60  
 56 gcagcccag cgcgccggca tccccgccgc ctctgcgcc gcgcgcgcc cccggcgccc 120  
 57 cctccccagc gcgccccgg cgcgtcctcc gcgcgcgcgt cgtcgccc atg gcc cgg 177  
 58 Met Ala Arg  
 59 1  
 61 gag aac ggc gag agc agc tcc tcc tgg aaa aag caa gct gaa gac atc 225  
 62 Glu Asn Gly Glu Ser Ser Ser Ser Trp Lys Lys Gln Ala Glu Asp Ile  
 63 5 10 15  
 65 aag aag atc ttc gag ttc aaa gag acc ctc gga acc ggg gcc ttt tcc 273

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66	Lys	Lys	Ile	Phe	Glu	Phe	Lys	Glu	Thr	Leu	Gly	Thr	Gly	Ala	Phe	Ser	
67	20					25					30					35	
69	gaa	gtg	gtt	tta	gct	gaa	gag	aag	gca	act	ggc	aag	ctc	ttt	gct	gtg	321
70	Glu	Val	Val	Leu	Ala	Glu	Glu	Lys	Ala	Thr	Gly	Lys	Leu	Phe	Ala	Val	
71					40					45					50		
73	aag	tgt	atc	cct	aag	aag	gcg	ctg	aag	ggc	aag	gaa	agc	agc	ata	gag	369
74	Lys	Cys	Ile	Pro	Lys	Lys	Ala	Leu	Lys	Gly	Lys	Glu	Ser	Ser	Ile	Glu	
75				55					60					65			
77	aat	gag	ata	gcc	gtc	ctg	aga	aag	att	aag	cat	gaa	aat	att	gtt	gcc	417
78	Asn	Glu	Ile	Ala	Val	Leu	Arg	Lys	Ile	Lys	His	Glu	Asn	Ile	Val	Ala	
79			70					75					80				
81	ctg	gaa	gac	att	tat	gaa	agc	cca	aat	cac	ctg	tac	ttg	gtc	atg	cag	465
82	Leu	Glu	Asp	Ile	Tyr	Glu	Ser	Pro	Asn	His	Leu	Tyr	Leu	Val	Met	Gln	
83		85					90				95						
85	ctg	gtg	tcc	ggt	gga	gag	ctg	ttt	gac	cgg	ata	gtg	gag	aag	ggg	ttt	513
86	Leu	Val	Ser	Gly	Gly	Glu	Leu	Phe	Asp	Arg	Ile	Val	Glu	Lys	Gly	Phe	
87	100					105				110					115		
89	tat	aca	gag	aag	gat	gcc	agc	act	ctg	atc	cgc	caa	gtc	ttg	gac	gcc	561
90	Tyr	Thr	Glu	Lys	Asp	Ala	Ser	Thr	Leu	Ile	Arg	Gln	Val	Leu	Asp	Ala	
91				120					125					130			
93	gtg	tac	tat	ctc	cac	aga	atg	ggc	atc	gtc	cac	aga	gac	ctc	aag	ccc	609
94	Val	Tyr	Tyr	Leu	His	Arg	Met	Gly	Ile	Val	His	Arg	Asp	Leu	Lys	Pro	
95			135					140					145				
97	gaa	aat	ctc	ttg	tac	tac	agt	caa	gat	gag	gag	tcc	aaa	ata	atg	atc	657
98	Glu	Asn	Leu	Leu	Tyr	Tyr	Ser	Gln	Asp	Glu	Glu	Ser	Lys	Ile	Met	Ile	
99		150					155					160					
101	agt	gac	ttt	gga	ttg	tca	aaa	atg	gag	ggc	aaa	gga	gat	gtg	atg	tcc	705
102	Ser	Asp	Phe	Gly	Leu	Ser	Lys	Met	Glu	Gly	Lys	Gly	Asp	Val	Met	Ser	
103		165					170					175					
105	act	gcc	tgt	gga	act	cca	ggc	tat	gtc	gct	cct	gaa	gtc	ctc	gcc	cag	753
106	Thr	Ala	Cys	Gly	Thr	Pro	Gly	Tyr	Val	Ala	Pro	Glu	Val	Leu	Ala	Gln	
107	180					185					190				195		
109	aaa	cct	tac	agc	aaa	gcc	gtt	gac	tgc	tgg	tcc	atc	gga	gtg	att	gcc	801
110	Lys	Pro	Tyr	Ser	Lys	Ala	Val	Asp	Cys	Trp	Ser	Ile	Gly	Val	Ile	Ala	
111				200					205					210			
113	tac	atc	ttg	ctc	tgc	ggc	tac	cct	cct	ttt	tat	gat	gaa	aat	gac	tcc	849
114	Tyr	Ile	Leu	Leu	Cys	Gly	Tyr	Pro	Pro	Phe	Tyr	Asp	Glu	Asn	Asp	Ser	
115			215					220					225				
117	aag	ctc	ttt	gag	cag	atc	ctc	aag	gcg	gaa	tat	gag	ttt	gac	tct	ccc	897
118	Lys	Leu	Phe	Glu	Gln	Ile	Leu	Lys	Ala	Glu	Tyr	Glu	Phe	Asp	Ser	Pro	
119			230				235					240					
121	tac	tgg	gat	gac	atc	tcc	gac	tct	gca	aaa	gac	ttc	att	cgg	aac	ctg	945
122	Tyr	Trp	Asp	Asp	Ile	Ser	Asp	Ser	Ala	Lys	Asp	Phe	Ile	Arg	Asn	Leu	
123		245					250				255						
125	atg	gag	aag	gac	ccg	aat	aaa	aga	tac	acg	tgt	gag	cag	gca	gct	cgg	993
126	Met	Glu	Lys	Asp	Pro	Asn	Lys	Arg	Tyr	Thr	Cys	Glu	Gln	Ala	Ala	Arg	
127	260					265				270					275		
129	cac	cca	tgg	atc	gct	ggt	gac	aca	gcc	ctc	aac	aaa	aac	atc	cac	gag	1041
130	His	Pro	Trp	Ile	Ala	Gly	Asp	Thr	Ala	Leu	Asn	Lys	Asn	Ile	His	Glu	

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```

131          280          285          290
133 tcc gtc agc gcc cag atc cgg aaa aac ttt gcc aag agc aaa tgg aga 1089
134 Ser Val Ser Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser Lys Trp Arg
135          295          300          305
137 caa gca ttt aat gcc acg gcc gtc gtg aga cat atg aga aaa cta cac 1137
138 Gln Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg Lys Leu His
139          310          315          320
141 ctc ggc agc agc ctg gac agt tca aat gca agt gtt tcg agc agc ctc 1185
142 Leu Gly Ser Ser Leu Asp Ser Ser Asn Ala Ser Val Ser Ser Ser Leu
143          325          330          335
145 agt ttg gcc agc caa aaa gac tgt gcg tat gta gca aaa cca gaa tcc 1233
146 Ser Leu Ala Ser Gln Lys Asp Cys Ala Tyr Val Ala Lys Pro Glu Ser
147 340          345          350          355
149 ctc agc tga cactgaagac gagcctggggg tggagaggag ggagccggca 1282
150 Leu Ser *
153 tctgccgagc acctcctgtt 'tgccaggcgc tttctatact taatcccatg tcatgcgacc 1342
154 ctaggacttt ttttaacatg taatcactgg gccgggtgca gtggctcacg cctgtaatcc 1402
155 caacactttg ggaggctgag gcaggaggac tggttgagtt caggagtttt aagaccagcc 1462
156 tgaccaacat ggtgaaaccc catctctact aaaatataaa aattagccgg gtgtggtggc 1522
157 gagcacctgt aatgtcagct acttgggagg ctgaggcagg agaatcactt gaaccaggga 1582
158 agcggagggt gcaatgagct gagatcacac cactgcactc cagcctgggt gacagattga 1642
159 gactccctct caaaaaaaaaa agggaaatca ttgaacactc gtggaaccct aggtattgca 1702
160 tattccattt acggtttggg aatccagggc tcaagtcctc gcaggggtac cgagctcgag 1762
161 atcgtaatca 1772
163 <210> SEQ ID NO: 2
164 <211> LENGTH: 357
165 <212> TYPE: PRT
166 <213> ORGANISM: Homo sapiens
168 <400> SEQUENCE: 2
169 Met Ala Arg Glu Asn Gly Glu Ser Ser Ser Ser Trp Lys Lys Gln Ala
170 1          5          10          15
171 Glu Asp Ile Lys Lys Ile Phe Glu Phe Lys Glu Thr Leu Gly Thr Gly
172          20          25          30
173 Ala Phe Ser Glu Val Val Leu Ala Glu Glu Lys Ala Thr Gly Lys Leu
174          35          40          45
175 Phe Ala Val Lys Cys Ile Pro Lys Lys Ala Leu Lys Gly Lys Glu Ser
176          50          55          60
177 Ser Ile Glu Asn Glu Ile Ala Val Leu Arg Lys Ile Lys His Glu Asn
178 65          70          75          80
179 Ile Val Ala Leu Glu Asp Ile Tyr Glu Ser Pro Asn His Leu Tyr Leu
180          85          90          95
181 Val Met Gln Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Val Glu
182          100          105          110
183 Lys Gly Phe Tyr Thr Glu Lys Asp Ala Ser Thr Leu Ile Arg Gln Val
184          115          120          125
185 Leu Asp Ala Val Tyr Tyr Leu His Arg Met Gly Ile Val His Arg Asp
186          130          135          140
187 Leu Lys Pro Glu Asn Leu Leu Tyr Tyr Ser Gln Asp Glu Glu Ser Lys
188 145          150          155          160

```

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```

189 Ile Met Ile Ser Asp Phe Gly Leu Ser Lys Met Glu Gly Lys Gly Asp
190           165           170           175
191 Val Met Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val
192           180           185           190
193 Leu Ala Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly
194           195           200           205
195 Val Ile Ala Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu
196           210           215           220
197 Asn Asp Ser Lys Leu Phe Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe
198 225           230           235           240
199 Asp Ser Pro Tyr Trp Asp Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile
200           245           250           255
201 Arg Asn Leu Met Glu Lys Asp Pro Asn Lys Arg Tyr Thr Cys Glu Gln
202           260           265           270
203 Ala Ala Arg His Pro Trp Ile Ala Gly Asp Thr Ala Leu Asn Lys Asn
204           275           280           285
205 Ile His Glu Ser Val Ser Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser
206           290           295           300
207 Lys Trp Arg Gln Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg
208 305           310           315           320
209 Lys Leu His Leu Gly Ser Ser Leu Asp Ser Ser Asn Ala Ser Val Ser
210           325           330           335
211 Ser Ser Leu Ser Leu Ala Ser Gln Lys Asp Cys Ala Tyr Val Ala Lys
212           340           345           350
213 Pro Glu Ser Leu Ser
214           355
217 <210> SEQ ID NO: 3
218 <211> LENGTH: 1074
219 <212> TYPE: DNA
220 <213> ORGANISM: Homo sapiens
222 <400> SEQUENCE: 3
223 atggcccggg agaacggcga gagcagctcc tcctggaaaa agcaagctga agacatcaag 60
224 aagatcttcg agttcaaaga gaccctcgga accggggcct tttccgaagt ggttttagct 120
225 gaagagaagg caactggcaa gctctttgct gtgaagtgtg tccctaagaa ggcgctgaag 180
226 ggcaaggaaa gcagcataga gaatgagata gccgtcctga gaaagattaa gcatgaaaaa 240
227 attgttgccc tggaagacat ttatgaaagc ccaaatcacc tgtacttggt catgcagctg 300
228 gtgtccggtg gagagctggt tgaccggata gtggagaagg ggttttatac agagaaggat 360
229 gccagcactc tgatccgcca agtcttggac gccgtgtact atctccacag aatgggcatc 420
230 gtccacagag acctcaagcc cgaaaatctc ttgtactaca gtcaagatga ggagtccaaa 480
231 ataataatgatca gtgacttttg attgtcaaaa atggaggggca aaggagatgt gatgtccact 540
232 gcctgtggaa ctccaggcta tgctgctcct gaagtcctcg ccagaaaacc ttacagcaaa 600
233 gccgttgact gctggtccat cggagtgtatt gcctacatct tgcctctgcg ctaccctcct 660
234 ttttatgatg aaaatgactc caagctcttt gagcagatcc tcaaggcgga atatgagttt 720
235 gactctccct actgggtgta catctccgac tctgcaaaaag acttcattcg gaacctgatg 780
236 gagaaggacc cgaataaaaag atacactgtg gagcaggcag ctcggcaccc atggatcgct 840
237 ggtgacacag ccctcaacaa aaacatccac gagtccgtca gcgccagat ccgaaaaaac 900
238 ttgccaaga gcaaatggag acaagcattt aatgccacgg ccgtcgtgag acatatgaga 960
239 aaactacacc tcggcagcag cctggacagt tcaaatgcaa gtgtttcgag cagcctcagt 1020
240 ttggccagcc aaaaagactg tgcgtatgta gcaaaaccag aatccctcag ctga 1074

```

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Input Set : A:\Sequence listing.txt

Output Set: N:\CRF4\10162002\J024036B.raw

```

242 <210> SEQ ID NO: 4
243 <211> LENGTH: 3579
244 <212> TYPE: DNA
245 <213> ORGANISM: Homo sapiens
247 <220> FEATURE:
248 <221> NAME/KEY: 5'UTR
249 <222> LOCATION: (1)...(1212)
251 <221> NAME/KEY: CDS
252 <222> LOCATION: (1213)...(3159)
W--> 254 <221> 3'UTR
255 <222> LOCATION: (3160)...(3579)
W--> 257 <400> 4
258 aacagttctg tcacttggtc gacatttaac acatgtgagt tgtatgaatg cctaaaggcc 60
259 ataccatgct gcctgggaaa cagcaagaac tccatcagtg gcagagacta tcactattat 120
260 tacattaaaa acaaccctga tatcaagcca gttgaaaatg gaccttgagg ggaaaaagta 180
261 cgagaaacca tgaaggatca agttcagcga aatgaggaca aatctactac cttgaaattg 240
262 gctgattttg gacttgcaaa gcatgtggtg agacctatat ttactgtgtg tgggacccca 300
263 acttacgtag ctcccgaat tctttctgag aaagggttat gactggaggt ggacatgtgg 360
264 gctgctggcg tgatcctcta tatcctgctg tgtggctttc cccattccg cagccctgag 420
265 agggaccagg acgagctctt taacatcatt cagctgggcc actttgagtt cctccccct 480
266 tactgggaca atatctctga tgctgctaaa gatctggtga gccggttgct ggtggtagac 540
267 cccaaaaagc gctacacagc tcatcaggtt cttcagcacc cctggatcga aacagctggc 600
268 aagaccaata cagtgaacg acagaagcag gtgtccccc gcagcgaggg tcacttccgg 660
269 agccagcaca agagggttgt ggagcaggta tcatatcygc tgagggtctca agatgtgtct 720
270 cttaaagccc caaattccca ctcaacttct catagccatt atgactgatt tagctgaata 780
271 accttgggac agcaaggcct atgtgacat tctctaaaat atttaagctc gagaatcaca 840
272 gacggaagc tgcaaggctc ctggctgcct gccagccgag ggaatctgga gaaaccattc 900
273 ctggggccgc gtggccccgt cgtgcccttg ttctgccctc ggaatggcct tcactcagca 960
274 catcctgaga acagccctct gaagcccagg gtctgaccc tagtgaagct ggggtgggcag 1020
275 cgccccgaa agatcactct gctcctcaac aggcgatcag tgcagacgtt cgagcagctc 1080
276 ttagctgaca tctcagaagc cttgggctct cccagatgga agaatgaccg tgtgaggaaa 1140
277 ctgtttaacc tcaagggcag ggaatcagg agcgtctctg atttcttcag ggaaggggat 1200
278 gctttcatag ct atg ggc aaa gaa cca ctg aca ctg aag agc att cag gtg 1251
279 Met Gly Lys Glu Pro Leu Thr Leu Lys Ser Ile Gln Val
280 1 5 10
282 gct gta gaa gaa ctg tac ccc aac aaa gcc cgg gcc ctg aca ctg gcc 1299
283 Ala Val Glu Glu Leu Tyr Pro Asn Lys Ala Arg Ala Leu Thr Leu Ala
284 15 20 25
286 cag cac agc cgt gcc cct tct cca agg ctg agg agc agg ctg ttt agc 1347
287 Gln His Ser Arg Ala Pro Ser Pro Arg Leu Arg Ser Arg Leu Phe Ser
288 30 35 40 45
290 aag gct ctg aaa gga gac cac cgc tgt ggg gag acc gag acc ccc aag 1395
291 Lys Ala Leu Lys Gly Asp His Arg Cys Gly Glu Thr Glu Thr Pro Lys
292 50 55 60
294 agc tgc agc gaa gtt gca gga tgc aag gca gcc atg agg cac cag ggg 1443
295 Ser Cys Ser Glu Val Ala Gly Cys Lys Ala Ala Met Arg His Gln Gly
296 65 70 75
298 aag atc ccc gag gag ctt tca cta gat gac aga gcg agg acc cag aag 1491
299 Lys Ile Pro Glu Glu Leu Ser Leu Asp Asp Arg Ala Arg Thr Gln Lys

```

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1,3,5,6  
Seq#:7; Xaa Pos. 3,5,8,10,11,13  
Seq#:8; Xaa Pos. 2,4,8,9  
Seq#:9; Xaa Pos. 2,4,8,9  
Seq#:10; Xaa Pos. 2,4

## VERIFICATION SUMMARY

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Input Set : A:\Sequence listing.txt

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L:35 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:38 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:42 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:46 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:50 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:54 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0  
L:254 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4  
L:257 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4  
L:589 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:593 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:597 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:601 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:606 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:610 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:614 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:618 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:622 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:626 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:632 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:637 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:642 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:646 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:651 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:654 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0  
L:670 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:674 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:678 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:682 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:686 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:689 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:693 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:697 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:701 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:705 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:709 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:710 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0  
L:723 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:727 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9  
L:731 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9  
L:735 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9  
L:739 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9  
L:742 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9  
L:746 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9  
L:750 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9  
L:754 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9  
L:758 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9

## VERIFICATION SUMMARY

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Input Set : A:\Sequence listing.txt

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L:762 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9  
L:766 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9  
L:767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0  
L:781 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:785 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10  
L:790 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10  
L:794 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10  
L:799 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10  
L:802 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10  
L:803 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0